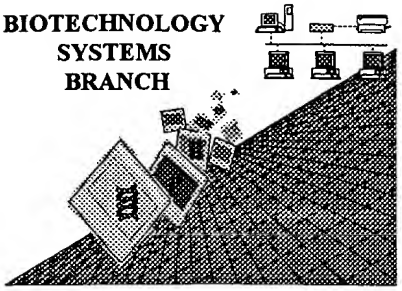
C. Kaufman

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/157,289B

Art Unit / Team No. : 1646

Date Processed by STIC: 08/03/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED **SUGGESTED CORRECTION** **SERIAL NUMBER:** 09/157,289B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of **n's** or **Xaa's** (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 ✓ Use of <220>Feature (NEW RULES)
Sequence(s) 3,5,6,7, maybe more are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/157,289B

DATE: 08/03/1999
TIME: 16:22:43

Input Set: I157289B.RAW

This Raw Listing contains the General Information Section and up to first 5 pages.

see page 5

<110> APPLICANT: ASHKENAZI, AVI J.
BOTSTEIN, DAVID
DODGE, KELLY H.
GURNEY, AUSTIN L.
KIM, KYUNG JIN
LAWRENCE, DAVID A.
PITTI, ROBERT
ROY, MARGARET A.
TUMAS, DANIEL B.
WOOD, WILLIAM I.
GENENTECH INC.
<120> TITLE OF INVENTION: DcR3 Polypeptide, A TNFR Homolog
<130> FILE REFERENCE: 11669.31US03
<140> CURRENT APPLICATION NUMBER: US/09/157,289B
<141> CURRENT FILING DATE: 1998-09-18
<150> EARLIER APPLICATION NUMBER: 60/059,288
<151> EARLIER FILING DATE: 1997-09-18
<150> EARLIER APPLICATION NUMBER: 60/094,640
<151> EARLIER FILING DATE: 1998-07-30
<160> NUMBER OF SEQ ID NOS: 16
<170> SOFTWARE: PatentIn Ver. 2.0
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<211> LENGTH: 300
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
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Thr Pro Thr Tyr Pro Trp Arg Asp Ala Glu Thr Gly Glu Arg Leu Val
         35                  40                  45
Cys Ala Gln Cys Pro Pro Gly Thr Phe Val Gln Arg Pro Cys Arg Arg
     50                  55                  60
Asp Ser Pro Thr Thr Cys Gly Pro Cys Pro Pro Arg His Tyr Thr Gln
 65                  70                  75                  80
Phe Trp Asn Tyr Leu Glu Arg Cys Arg Tyr Cys Asn Val Leu Cys Gly
                 85                  90                  95
Glu Arg Glu Glu Glu Ala Arg Ala Cys His Ala Thr His Asn Arg Ala
            100                 105                 110
Cys Arg Cys Arg Thr Gly Phe Phe Ala His Ala Gly Phe Cys Leu Glu
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His Ala Ser Cys Pro Pro Gly Ala Gly Val Ile Ala Pro Gly Thr Pro
    130                 135                 140
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Ser Gln Asn Thr Gln Cys Gln Pro Cys Pro Pro Gly Thr Phe Ser Ala
145 150 155 160
Ser Ser Ser Ser Ser Glu Gln Cys Gln Pro His Arg Asn Cys Thr Ala
165 170 175
Leu Gly Leu Ala Leu Asn Val Pro Gly Ser Ser Ser His Asp Thr Leu
180 185 190
Cys Thr Ser Cys Thr Gly Phe Pro Leu Ser Thr Arg Val Pro Gly Ala
195 200 205
Glu Glu Cys Glu Arg Ala Val Ile Asp Phe Val Ala Phe Gln Asp Ile
210 215 220
Ser Ile Lys Arg Leu Gln Arg Leu Leu Gln Ala Leu Glu Ala Pro Glu
225 230 235 240
Gly Trp Gly Pro Thr Pro Arg Ala Gly Arg Ala Ala Leu Gln Leu Lys
245 250 255
Leu Arg Arg Arg Leu Thr Glu Leu Leu Gly Ala Gln Asp Gly Ala Leu
260 265 270
Leu Val Arg Leu Leu Gln Ala Leu Arg Val Ala Arg Met Pro Gly Leu
275 280 285
Glu Arg Ser Val Arg Glu Arg Phe Leu Pro Val His
290 295 300

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aggcctgtcg ctgctgtgcc tggtgttggc gctgcctgcc ctgctgccgg tgccggctgt 180
acgcggagtg gcagaaacac ccacctaccc ctggcgggac gcagagacag gggagcggct 240
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cacccacaac cgtgcctgcc gctgccgcac cggcttcttc gcgcacgctg gtttctgctt 480
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gctggagcgg agcgtccgtg agcgcttcct ccctgtgcac tgatcctggc cccctcttat 1020
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<211> LENGTH: 491

see item 12 on Error summary sheet

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116         gggcttgcca cgccacccac aaccgtgcct gccgctgccg caccggcttc ttcgcgcacg 180
117         ctggtttctg cttggagcac gcatcgtgtc cacctggtgc cggcgtgatt gccccgggca 240
118         cccccagcca gaacacgcag tgcctagccg tgcccccccag gcaccttctc agccagcagc 300
119         tccagctcag agcagtgcca gccccaccgc aactgcacgg ccctgggcct ggccctcaat 360
120         gtgccaggct cttcctccca tgacaccctg tgcaccagct gcactggctt ccccctcagc 420
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133         ctacctggag cgc                                                    73
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169   <223> OTHER INFORMATION: n = any nucleotide
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W--> 192   antaactgga gcnctgccgc tactgnaacg tcctctgngg ggagcntgag gaggaggcan 120
W--> 193   gngcttgcca cgccacccac aaccgcgcct gcngctgcag caccggnttc ttcgcgcacg 180
W--> 194   ctgntttctg cttggagcac gcatcgtgtc cacctggtgn cggcgtgatt gcnccgggca 240
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```
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199     <213> ORGANISM: Unknown
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202     <222> LOCATION: (182)
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206          ggaggaggca cgggcttgcc acgccaccca caaccgtgcc tgccgctgcc gcaccggctt 120
207          cttcgcgcac gctggtttct gcttggagca cgcatcgtgt ccacctggtg ccggcgtgat 180
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W--> 220          acccccagcc agaacacgca gnccagccgt gccccccagg caccttctca gccagcagct 180
221          ccagctcaga gcagtgccag ccccaccgca actgcacggc cctgggcctg gccctcaatg 240
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243     <223> OTHER INFORMATION: n = any nucleotide
244     <220> FEATURE:
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION **US/09/157,289B**

DATE: 08/03/1999
TIME: 16:22:43

Input Set: **I157289B.RAW**

Line	?	Error/Warning	Original Text
92	W	"N" or "Xaa" used: Feature required	atgaggtttn ttaaaaaaaa aaaaaaaaaa aaaa
115	W	"N" or "Xaa" used: Feature required	antaactgga gcnctgccgc tactgnaacg tcctctgn
191	W	"N" or "Xaa" used: Feature required	gccgagacag ccccacgacg tgtggcccgt gtccaccg
192	W	"N" or "Xaa" used: Feature required	antaactgga gcnctgccgc tactgnaacg tcctctgn
193	W	"N" or "Xaa" used: Feature required	gngcttgcca cgccacccac aaccgcgcct gcngctgc
194	W	"N" or "Xaa" used: Feature required	ctgntttctg cttggagcac gcatcgtgtc cacctggt
208	W	"N" or "Xaa" used: Feature required	tnccccgggc acccccagcc a
220	W	"N" or "Xaa" used: Feature required	acccccagcc agaacacgca gnccagccgt gcccccca
257	W	"N" or "Xaa" used: Feature required	agcngtgcnc cncaggcacc ttctcagcca gcagttcc
259	W	"N" or "Xaa" used: Feature required	cgctgtgcac cagctgcact ggcttccccc tcagcacc
278	W	"N" or "Xaa" used: Feature required	cttgtccacc tggtgccggc gtgattnccc gggcaccc
279	W	"N" or "Xaa" used: Feature required	gccntccccc caggcacctt ctcagccagc agctccag
280	W	"N" or "Xaa" used: Feature required	cgcaactgca acgccctggn ctggccctca atgtgcca